



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/018,730A

DATE: 06/06/2002  
TIME: 12:55:54

Input Set : A:\P02353US1.txt  
Output Set: N:\CRF3\06062002\J018730A.raw

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3 <110> APPLICANT: Luet, Wong  
4 Jonathan, Jones  
6 <120> TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS  
8 <130> FILE REFERENCE: P02353US1 / 10112404 / N.7627.7B  
10 <140> CURRENT APPLICATION NUMBER: US 10/018,730A  
C--> 11 <141> CURRENT FILING DATE: 2002-04-04  
13 <150> PRIOR APPLICATION NUMBER: GB 9914373.7  
14 <151> PRIOR FILING DATE: 1999-06-18  
16 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02379  
17 <151> PRIOR FILING DATE: 2000-06-19  
19 <160> NUMBER OF SEQ ID NOS: 18  
21 <170> SOFTWARE: PatentIn version 3.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1242  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Pseudomonas putida  
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33 gcctggcag ttctgcaga atcaaacgtt ccggatctgg tggactcg ctgcaacggc 180  
35 ggacactgga tcgcccactcg cgccaaactg atccgtgagg cctatgaaga ttaccggcac 240  
37 tttccagcg agtgcgggtt catccctcgat gaagccggcg aagcctacga cttcattccc 300  
39 acctcgatgg atccggccga gcaagcggcaat tticgtgcgc tggccacca agtggttggc 360  
41 atgcccgtgg tggataagct ggagaaccgg atccaggagc tggcctgctc gctgatcgag 420  
43 agcctgcgccc cgcaaggaca gtcgaacttc accgaggact acgcccgaacc cttcccgata 480  
45 cgcatttcata tgctgtcgat agtctaccg gaagaagata tcccgactt gaaataccta 540  
47 acggatcaga tgaccgtcc ggtatggcagc atgacccatcg cagaggccaa ggaggcgctc 600  
49 tacgactatac tgataccatcatcgacaa cgccggcaga agccgggaac cgacgtatc 660  
51 agcatcggtt ccaacggcca ggtcaatggg cgaccatca ccagtgcacg agccaagagg 720  
53 atgtgtggcc tggatgtggcgtt cggcggcctg gatacggtgg tcaatttcct cagcttcagc 780  
55 atggagttcc tggccaaaag cccggagcat cgccaggagc tgatcgagcg tcccgagcgt 840  
57 attccagccg cttgcgagga actactccgg cgcttctcg tgggttgcga tggccgcata 900  
59 ctcaccccg attacgagtt tcatggcgatg caactgaaga aagggtgacca gatccctgcta 960  
61 ccgcagatgc tggatgtggcgtt ggtatggcgatc gaaaacgcct gcccgtatcg cgtcgacttc 1020  
63 agtgcggaaa aggtttcaca caccacccatgg ggcacggca gccatctgtg ctttggccag 1080  
65 cacctggccc gcccggaaat catcgatcacc cttcaaggaat ggctgaccag gattccgtac 1140  
67 ttctccatttgc ccccggtgc ccagattcag cacaagagcg gatcgatcg cggcgatcg 1200  
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74 <212> TYPE: PRT  
75 <213> ORGANISM: Pseudomonas putida  
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79 Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro  
80 1 5 10 15  
83 His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser  
84 20 25 30  
87 Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser  
88 35 40 45  
91 Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile  
92 50 55 60  
95 Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His  
96 65 70 75 80  
99 Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr  
100 85 90 95  
103 Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg  
104 100 105 110  
107 Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu  
108 115 120 125  
111 Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro  
112 130 135 140  
115 Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile  
116 145 150 155 160  
119 Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His  
120 165 170 175  
123 Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr  
124 180 185 190  
127 Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile  
128 195 200 205  
131 Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala  
132 210 215 220  
135 Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg  
136 225 230 235 240  
139 Met Cys Gly Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe  
140 245 250 255  
143 Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln  
144 260 265 270  
147 Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu  
148 275 280 285  
151 Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp  
152 290 295 300  
155 Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu  
156 305 310 315 320  
159 Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met  
160 325 330 335  
163 His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His  
164 340 345 350  
167 Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile  
168 355 360 365  
171 Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala  
172 370 375 380  
175 Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln

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273	aaacaagcaa	gcatcacgg	cagcggttgc	tcaggagaag	cgtggagcgg	atatggagaa	2580										
275	tataaaggaa	ttgcgtcgaa	ctatcttgc	gagctgcaag	aaggagatac	gattacgtgc	2640										
277	tttatttcca	caccgcagtc	agaatttacg	ctgccaaaag	accctgaaac	gccgcttatac	2700										
279	atggcggac	cggAACAGG	cgtcgcccg	tttagaggct	ttgtgcaggc	gcgaaacag	2760										
281	ctaaaagaac	aaggacagtc	acttggagaa	gcacattat	acttcggctg	ccgttacact	2820										
283	catgaagact	atctgtatca	agaagagctt	gaaaacgccc	aaagcgaagg	catcattacg	2880										
285	cttcataccg	cttttctcg	catgccaaat	cagccgaaaa	catacgta	gcacgtaatg	2940										
287	gaacaagacg	gcaagaaatt	gattgaactt	cttgatcaag	gagcgcactt	ctatattgc	3000										
289	ggagacggaa	gccaaatggc	acctgccgtt	gaagcaacgc	ttatgaaaag	ctatgctgac	3060										
291	gttcaccaag	tgagtgaagc	agacgctcg	ttatggctgc	agcagctaga	agaaaaaggc	3120										
293	cgatacgcaa	aagacgtgt	ggctggtaa				3150										
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297	<211>	LENGTH:	1049														
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308					20				25			30					
311	Ile	Ala	Asp	Glu	Leu	Gly	Glu	Ile	Phe	Lys	Phe	Glu	Ala	Pro	Gly	Arg	
312					35				40			45					
315	Val	Thr	Arg	Tyr	Leu	Ser	Ser	Gln	Arg	Leu	Ile	Lys	Glu	Ala	Cys	Asp	
316					50				55			60					
319	Glu	Ser	Arg	Phe	Asp	Lys	Asn	Leu	Ser	Gln	Ala	Leu	Lys	Phe	Val	Arg	
320					65				70			75			80		
323	Asp	Phe	Ala	Gly	Asp	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	
324					85				90			95					
327	Trp	Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	
328					100				105			110					
331	Met	Lys	Gly	Tyr	His	Ala	Met	Met	Val	Asp	Ile	Ala	Val	Gln	Leu	Val	
332					115				120			125					
335	Gln	Lys	Trp	Glu	Arg	Leu	Asn	Ala	Asp	Glu	His	Ile	Glu	Val	Pro	Glu	
336					130				135			140					
339	Asp	Met	Thr	Arg	Leu	Thr	Leu	Asp	Thr	Ile	Gly	Leu	Cys	Gly	Phe	Asn	
340					145				150			155			160		
343	Tyr	Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	
344					165				170			175					
347	Ser	Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	
348					180				185			190					
351	Asn	Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	
352					195				200			205					
355	Asp	Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	
356					210				215			220					
359	Lys	Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	
360					225				230			235			240		
363	Gly	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	
364					245				250			255					

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367 Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly  
 368 260 265 270  
 371 Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu  
 372 275 280 285  
 375 Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Ala Pro  
 376 290 295 300  
 379 Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn  
 380 305 310 315 320  
 383 Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala  
 384 325 330 335  
 387 Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp  
 388 340 345 350  
 391 Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp  
 392 355 360 365  
 395 Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser  
 396 370 375 380  
 399 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala  
 400 385 390 395 400  
 403 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly  
 404 405 410 415  
 407 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu  
 408 420 425 430  
 411 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys  
 412 435 440 445  
 415 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr  
 416 450 455 460  
 419 Glu Gln Ser Ala Lys Lys Ala Arg Lys Lys Ala Glu Asn Ala His Asn  
 420 465 470 475 480  
 423 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly  
 424 485 490 495  
 427 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro  
 428 500 505 510  
 431 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly  
 432 515 520 525  
 435 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn  
 436 530 535 540  
 439 Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val  
 440 545 550 555 560  
 443 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala  
 444 565 570 575  
 447 Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala  
 448 580 585 590  
 451 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp  
 452 595 600 605  
 455 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp  
 456 610 615 620  
 459 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys  
 460 625 630 635 640  
 463 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu

**VERIFICATION SUMMARY**

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date